

Figure 1

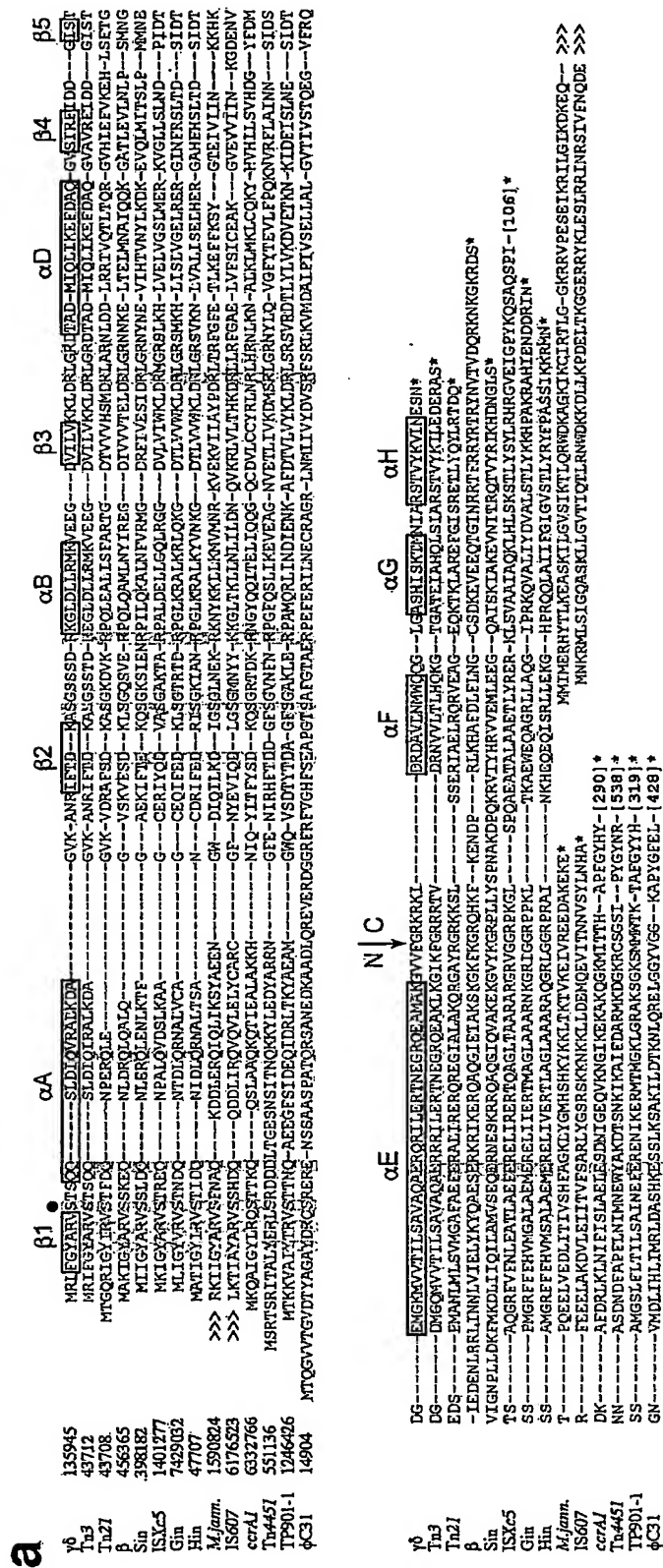
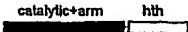





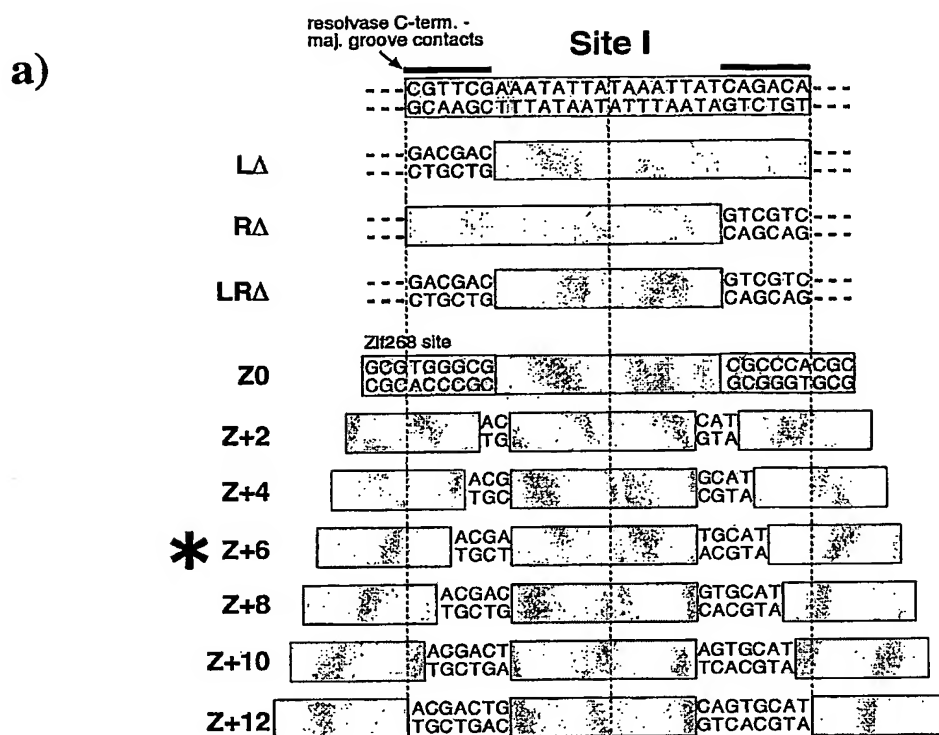
Figure 1 cont..

b

	transposon resolvase plasmid resolvase DNA Invertase	Tn3, $\gamma\delta$ , Tn21 Sin, $\beta$ Gin, Hin
	transposon resolvase	ISXc5
	Integrase transposase	$\phi$ C31, TP901-1 Tn4451, SSCmec (CcrA1)
	transposase	IS507, M.Jann. (MJ0014)

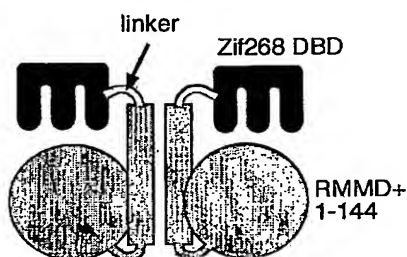
10/529059

Figure 2



b)

## Z-resolvase



## Linker sequences:

TVDRSSDPTSQ (confection)

GSGGSG

GSGGSGGSG

\* GSGGSGGSGGSG

GGGSGGG

GGGSGGGGSGGG

NRVAQQLAGKQS (a la LacI)

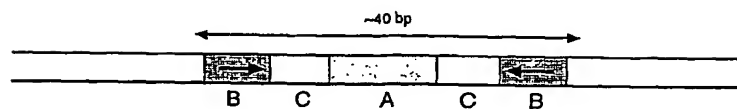
SDYTQNNIHP (a la T4 Endo VII)

TVDRTS

TS

10/529059

## A generic hybrid recombination site



A. The central sequence - Interacts with catalytic domain and linker. Protein sequence may need to be optimized for any chosen sequence.

B. Sequence motifs recognized by the DNA-binding domain. If they are the same, they must be in inverted repeat, as shown. For Zif269, the sequence is 9 bp long.

C. Spacer sequence. No known sequence requirements at present, but length is important to optimize positions of B motifs.

**Figure 3**

10/529059

Figure 4

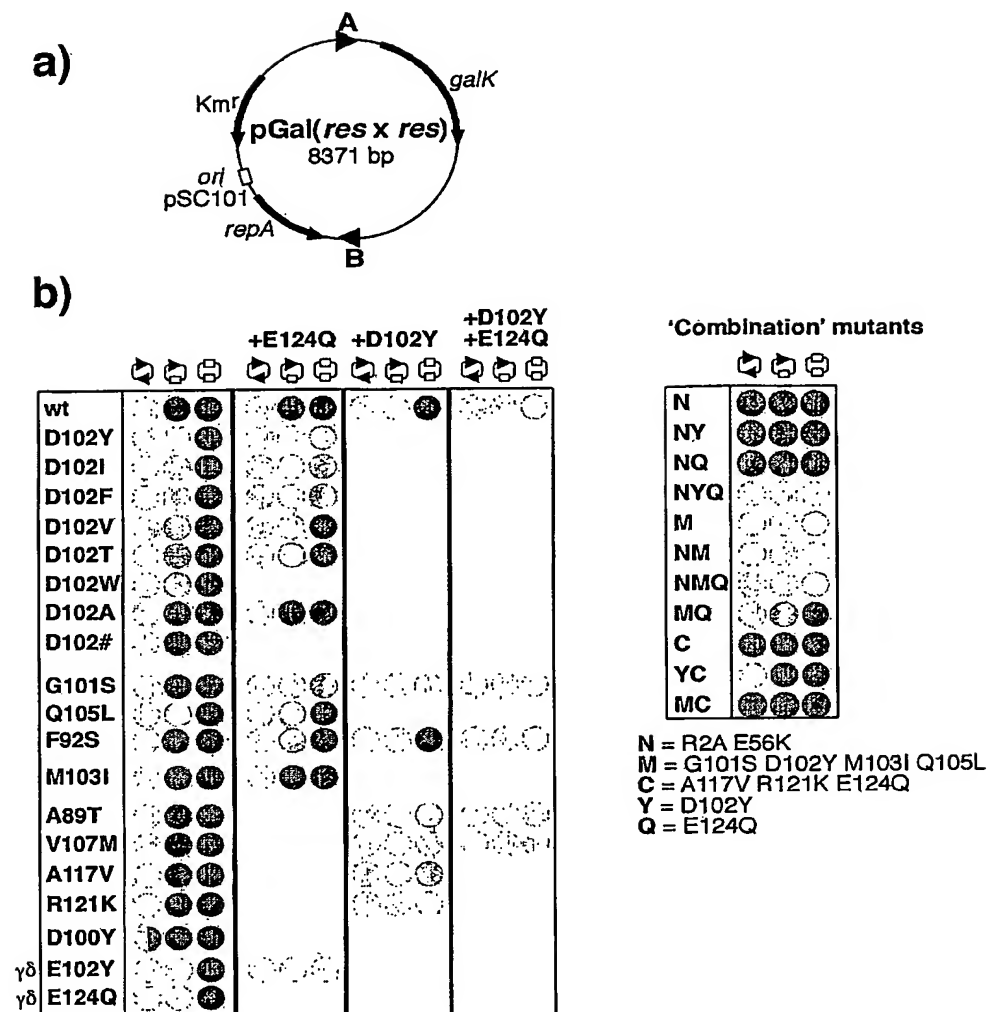


Figure 4 cont..

c)

		+D102Y	+E124Q	+D102Y +E124Q
wt				
D102I				
D102F				
D102V				
D102T				
D102W				
D102A				
D25G				
M53T				
L66I				
L66F				
G70A				
G70C				
D75V				
M76V				
I77T				
A89T				
F92S				
T99S				
G101S				
G101C				
M103I				
M103V				
Q105L				
V107M				
I109I				
A117V				
R121K				
R121M				
R121S				
I138V				

N	
NY	
NQ	
NYQ	
M	
MQ	
NM	
NMQ	
C	
YC	
MC	

N = R2A E56K  
 M = G101S D102Y M103I Q105L  
 C = A117V R121K E124Q  
 Y = D102Y  
 Q = E124Q

10/529059

Figure 5




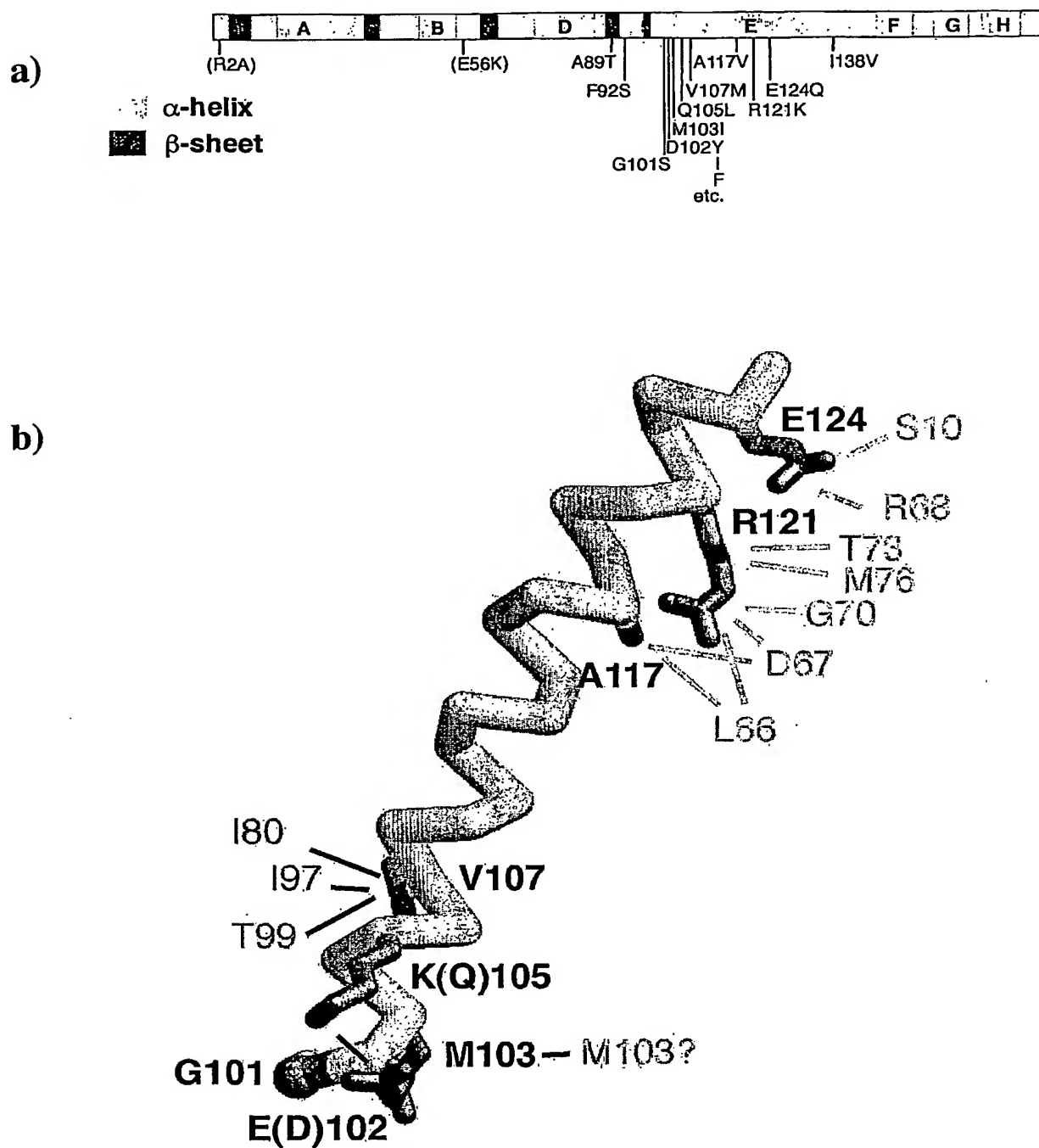
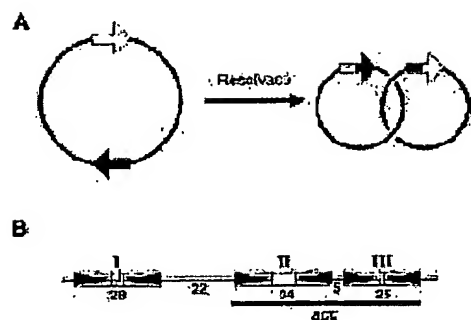
	<i>in vitro</i>			2 x 1 complex
				
wt				
N	-	-	-	
NYQ	++++	++++	++++	
M	++++	+++	++	
NM	++	+++	++++	++++
NMQ	++	+++	++++	++++
MQ	++	+++	++++	
C	++++	-	-	
YC	++++	N.D.	+	
MC	++++	N.D.	+	

Figure 6





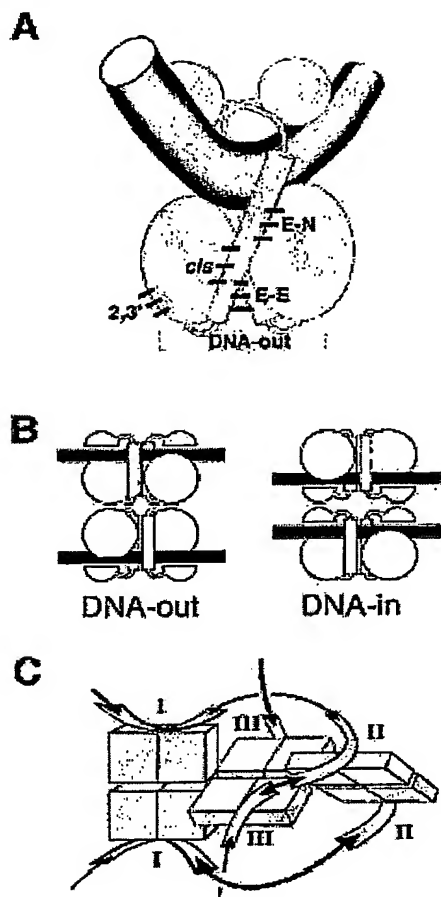
Type 1 ☒ Hypothetical DNA-aid interface  
Type 2 ☐ C<sub>1</sub> 1-2 interface  
          ☒ C<sub>1</sub> 2-3, but not 1-2 interface  
Type 3 ☐ C<sub>1</sub> 2-3' interface  
          ☐ Other  
          ☒ Ser-10



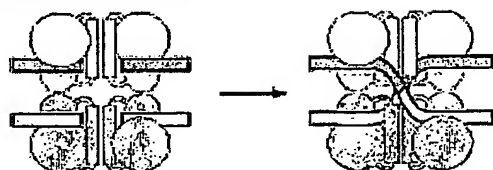
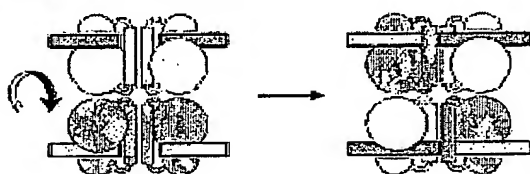
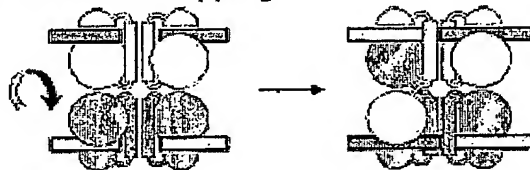
**Figure 7**

10/529059

Figure 8



10/529059

**Figure 9****A fixed subunits****B subunit rotation****C domain swapping**

10/529059

Figure 10

From:	Assay	Method	amino acids	(Additional) mutations	Phenotype
wt					
	pGal(res x 1)	oligo oligo	1-21 94-121	none found D102Y D102Y A113T D102A M103I D102Y Q116H D102I M103W I97V G101S D102Y A113T D102Y	
		PCR-OG	10-140		
D102Y					
	pGal(1 x 1)	oligo PCR	1-21 1-185	none found L66F L66I G70A G70C I77T F92S T99S M103I M103V Q105L R121M R121S D25G M76V D25G G101C M53T D75V I01V M103I I77T L123I F92C T109I R121K E124Q A117V H38V	
		PCR-OG	114-140		
E124Q					
	pGal(res x 1)	oligo	94-121	D102Y G101S Q105L U102V M103W H119H	
		PCR-OG	10-140	G101S D102V Q105L D102V F92S	
		PCR-ver PCR-dP	10-140 10-92		
DY/EQ					
	p3u(1 x 1)	PCR	1-185	A89T G101S V107M	

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